

FIGURE 1

GGACTAATCTGTGGGAGCAGTTTATTCCAGTATCACCCAGGGTGCAGCCACACCAGGACTGT
GTTGAAGGGTGTCTTTCTTTTAAATGTAATACCTCCTCATCTTTCTTTACACAGTG
TCTGAGAACATTTACATTATAGATAAGTAGTACATGGTGGATAACTTCTACTTTTAGGAGGA
CTACTCTCTTCTGACAGTCCTAGACTGGTCTTCTACACTAAGACACCATGAAGGAGTATGTG
CTCCTATTATTCTGGCTTTGTGCTCTGCCAAACCCTTCTTTAGCCCTTCACACATCGCACT
GAAGAATATGATGCTGAAGGATATGGAAGACACAGATGATGATGATGATGATGATGATG
ATGATGATGATGAGGACAACCTCTCTTTTCCAACAAGAGAGCCAAGAAGCCATTTTTTTCCA
TTTGATCTGTTTCCAATGTGTCCATTTGGATGTCAGTGCTATTACAGAGTTGTACATTGCTC
AGATTTAGGTTTGACCTCAGTCCCAACCAACATTCCATTTGATACTCGAATGCTTGATCTTC
AAAACAATAAAATTAAGGAAATCAAAGAAAATGATTTTAAAGGACTCACTTCACTTTATGGT
CTGATCCTGAACAACAAGCTAACGAAGATTCACCCAAAAGCCTTTCTAACCACAAAGAA
GTTGCGAAGGCTGTATCTGTCCCAATCAACTAAGTGAAATACCACTTAATCTTCCCAAAT
CATTAGCAGAACTCAGAATTCATGAAAATAAAGTTAAGAAAATACAAAAGGACACATTCAAA
GGAATGAATGCTTTACACGTTTGGAAATGAGTGCAAACCCTCTTGATAATAATGGGATAGA
GCCAGGGGCATTTGAAGGGGTGACGGTGTTCATATCAGAATTGCAGAAGCAAACTGACCT
CAGTTCCTAAAGGCTTACCACCAACTTTATTGGAGCTTCACTTAGATTATAATAAAATTTCA
ACAGTGGAACCTTGAGGATTTTAAACGATACAAAGAACTACAAAGGCTGGGCCTAGGAAACAA
CAAAATCACAGATATCGAAAATGGGAGTCTTGCTAACATACCACGTGTGAGAGAAATACATT
TGGAACAATAAACTAAAAAAATCCCTTCAGGATTACCAGAGTTGAAATACCTCCAGATA
ATCTTCCTTCATTCTAATTCAATTGCAAGAGTGGGAGTAAATGACTTCTGTCCAACAGTGCC
AAAGATGAAGAAATCTTTATACAGTGCAATAAGTTTATTCAACAACCCGGTGAAATACTGGG
AAATGCAACCTGCAACATTTCTGTGTGTTTTGAGCAGAATGAGTGTTGAGCTTGGGAACCTTT
GGAATGTAATAATTAGTAATTGGTAATGTCCATTTAATATAAGATTCAAAAATCCCTACATT
TGGAATACTTGAACCTCTATTAATAATGGTAGTATTATATATACAAGCAAATATCTATTCTCA
AGTGGTAAGTCCACTGACTTATTTTATGACAAGAAATTTCAACGGAATTTTGCCAACTATT
GATACATAAGGGGTTGAGAGAAACAAGCATCTATTGCAGTTTCCTTTTTGCGTACAAATGAT
CTTACATAAATCTCATGCTTGACCATTCTTTCTTCATAACAAAAAGTAAGATATTCGGTA
TTTAACACTTTGTATCAAGCACATTTTAAAAAGAACTGTACTGTAAATGGAATGCTTGACT
TAGCAAAATTTGTGCTCTTTTCATTTGCTGTTAGAAAAACAGAATTAACAAAGACAGTAATGT
GAAGAGTGCAATTACACTATTCTTATTCTTTAGTAACTTGGGTAGTACTGTAATATTTTAAAT
CATCTTAAAGTATGATTTGATATAATCTTATTGAAATTACCTTATCATGTCTTAGAGCCCGT
CTTTATGTTTAAACTAATTTCTTAAAAATAAAGCCTTCAGTAAATGTTTATTACCAACTTGA
TAAATGCTACTCATAAGAGCTGGTTTGGGGCTATAGCATATGCTTTTTTTTTTTTAAATTATT
ACCTGATTTAAAAATCTCTGTAAAAACGTGTAGTGTTCATAAAATCTGTAACTCGCATTTT
AATGATCCGCTATTATAAGCTTTTAAATAGCATGAAAATTGTTAGGCTATATAACATTGCCAC
TTCAACTCTAAGGAATATTTTTGAGATATCCCTTTGGAAGACCTTGCTTGGAAGAGCCTGGA
CACTAACAATTTCTACACCAAATTGTCTCTTCAAATACGTATGGACTGGATAACTCTGAGAAA
CACATCTAGTATAACTGAATAAGCAGAGCATCAAATTAAACAGACAGAAACCGAAAGCTCTA
TATAAATGCTCAGAGTTCTTTATGTATTTCTTATTGGCATTCAACATATGTAAAATCAGAAA
ACAGGGAAATTTTCATTAAAAATATTGGTTTGAAAT

FIGURE 2

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA34392

<subunit 1 of 1, 379 aa, 1 stop

<MW: 43302, pI: 7.30, NX(S/T): 1

MKEYVLLLFLALCSAKPFFSPSHIALKNMMLKDMEDTDDDDDDDDDDDDDEDNSLFPTREPR
SHFFPFDLFPMCPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGL
TSLYGLILNNKLTKEIHPKAFLTTKKLRRLLYLSHNQLSEIPLNLPKSLAELRIHENKVKKIQ
KDTFKGMNALHVLEMSANPLDNNGIEPGAEGVTVFHIRIAEAKLTSVPKGLPPTLLELHLD
YNKISTVELEDFKRYKELQRLGLGNNKITDIENGLANIPRVREIHLNENKLLKIPSGLPPEL
KYLQIIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAISLFNNPVKYWEMQPATFRCVLSRMSV
QLGNFGM

Signal sequence.

amino acids 1-15

N-glycosylation site.

amino acids 281-285

N-myristoylation sites.

amino acids 129-135, 210-216, 214-220, 237-243, 270-276, 282-288

Leucine zipper pattern.

amino acids 154-176

0944920 "033101
T07E80" 6264660

FIGURE 3

CGGACGCGTGGGCGGACGCGTGGGCCCCGSGCACCGCCCCCGGCCCGGCCCTCCGCCCTCCGCACTCGCGCCTCC
CTCCCTCCGCCCGCTCCCGCGCCCTCCTCCCTCCCTCCTCCCCAGCTGTCCCGTTTCGCGTCAATGCCGAGCCTCCC
GGCCCCGCGGCCCGCTGCTGCTCCTCGGGTGTGCTGCTCGGCTCCCGGCCGGCCCGCGGCCCGGCCAGGA
GCCCCCGTGTGCTGCCATCCGTTCTGAGAAGGAGCGCTGCCCGTTTCGGGGAGCGGCAGGCTGCACCTTCGGCGG
GAAGGTCTATGCCTTGGACGAGACGTGGCACCCGGACCTAGGGCAGCCATTTCGGGGTGATGCGCTGCGTGTGTG
CGCCTGCGAGGCGCCTCAGTGGGGTGCCTGTACCAGGGGCCCTGGCAGGGTCACTGCAAGAATCAAACCAGAA
GTGCCCCAACCCCGCCCTGTGGGCAGCCGCGCCAGCTGCCGGGACACTGCTGCCAGACCTGCCCCAGGAGCGCAG
CAGTTCGGAGCGGCAGCCGAGCGGCCTGTCTTCGAGTATCCGCGGGACCCGGAGCATCGCAGTTATAGCGACCG
CGGGGAGCCAGGCGCTGAGGAGCGGGCCCGTGGTGACGGCCACACGGACTTCGTGGCGCTGCTGACAGGGCCGAG
GTCGCAGGCGGTGGCACGAGCCCGAGTCTCGCTGCTGCGCTCTAGCCTCCGCTTCTCTATCTCCTACAGGCGGCT
GGACCGCCCTACCAGGATCCGCTTCTCAGACTCCAATGGCAGTGTCTGTTTGAGCACCTGCAGCCCCCACCACA
AGATGGCCTGGTCTGTGGGGTGTGGCGGGCAGTGCCTCGGTTGTCTCTGCGGCTCCTTAGGGCAGAACAGCTGCA
TGTGGCACTTGTGACACTCACTCACCTTCAGGGGAGGTCTGGGGGCCCTCTCATCCGGCACCGGGGCCCTGGCTGC
AGAGACCTTCAGTGCCATCCTGACTCTAGAAGGCCCCCACAGCAGGGCGTAGGGGGCATCACCTGCTCACTCT
CAGTGACACAGAGGACTCCTTGCAATTTTTGCTGCTCTTCCGAGGGCTGCTGGAACCCAGGAGTGGGGGACTAAC
CCAGGTTCCCTTGAGGCTCCAGATTCTACACCAGGGGCAGCTACTGCGAGAACTTCAGGCCAATGTCTCAGCCCCA
GGAACCCGCTTTGCTGAGGTGCTGCCAACCTGACAGTCCAGGAGATGGACTGGCTGGTGTGCTGGGGGAGCTGCA
GATGGCCCTGGAGTGGGCAGGCAGGGCTGCGCATCAGTGGACACATTGCTGCCAGGAAGAGCTGCGACGT
CCTGCAAAGTGTCTTTGTGGGGCTGATGCCCTGATCCCACTCCAGACGGGTGCTGCCGGCTCAGCCAGCCCTCAC
GCTGCTAGGAAATGGCTCCCTGATCTATCAGGTGCAAGTGGTAGGGACAAGCAGTGAGGTGGTGGCCATGACACT
GGAGACCAAGCCTCAGCGGAGGGATCAGCGCACTGTCTGTGCCACATGGCTGGACTCCAGCCAGGAGGACACAC
GGCGTGGGTATCTGCCCTGGGCTGGGTGCCCGAGGGGGCTCATATGCTGCTGCAGAATGAGCTCTTCTGAACGT
GGGACCAAGGACTTCCCAGACGGAGAGCTTCGGGGGCAGTGGCTGCCCTGCCCTACTGTGGGCATAGCGCCCCG
CCATGACACGCTGCCCCGTGCCCTTAGCAGGAGCCCTGGTGTACCCCCCTGTGAAGAGCCAAGCAGCAGGGCACGC
CTGGCTTTCTTGGATACCCACTGTCACTGTCACTATGAAGTGTGCTGGCTGGGCTTGGTGGCTCAGAACAAGG
CACTGTCACTGCCCACCTCCTTGGGCCTCCTGGAACGCCAGGGCCTCGGCGGCTGCTGAAGGGATTCTATGGCTC
AGAGGCCCAGGGTGTGGTGAAGGACCTGGAGCCGGAAGTGTGCGGCACCTGGCAAAAGGCATGGCCTCCCTGAT
GATCACCAACAGGGTAGCCCCAGAGGGGAGCTCCGAGGGCAGGTGCACATAGCCAACCAATGTGAGGTGGCGG
ACTGCGCCTGGAGGCGGCCGGGGCCGAGGGGGTGCGGGCGCTGGGGGCTCCGGATACAGCCTCTGCTGCGCCGCC
TGTGGTGCCTGGTCTCCCGGCCCTAGCGCCCGCCAAACCTGGTGGTCTTGGGCGGCCCCGAGACCCCAACACATG
CTTCTTCGAGGGGCAGCAGCGCCCCCACGGGGCTCGCTGGGCGCCCAACTACGACCCGCTCTGCTCACTCTGCAC
CTGCCAGAGACGAACGGTGATCTGTGACCCGGTGGTGTGCCACCGCCAGCTGCCACACCCGGTGCAGGCTCC
CGACCACTGCTGCCCTGTTTGCCCTGAGAAACAAGATGTGAGAGACTTGCCAGGGCTGCCAAGGAGCCGGGACCC
AGGAGAGGGCTGCTATTTTGTGTTGACCGGAGCTGGCGGGCAGCGGTACGCGGTGGCACCCCGTTGTGCCCCC
CTTTGGCTTAATTAAGTGTGCTGTCTGCACCTGCAAGGGGGGCACTGGAGAGGTGCACTGTGAGAAGGTGCAGTG
TCCCCGGCTGGCCTGTGCCAGCCTGTGCGTGTCAACCCACCGACTGCTGCAACAGTGTCCAGTGGGGTGGG
GGCCACCCCCAGCTGGGGGACCCCATGCAGGCTGATGGGCCCCGGGGCTGCCGTTTTGCTGGGCAGTGGTTCCC
AGAGAGTCAGAGCTGGCACCCCTCAGTGCCCCCTTTTGGAGAGATGAGCTGTATCACCTGCAGATGTGGGGCAGG
GGTGCTCACTGTGAGCGGGATGACTGTTCACTGCCACTGTCTGTGGCTCGGGGAAGGAGAGTCGATGCTGTTT
CCGCTGCACGGCCCCACCGCGGCCCCAGAGACCAGAACTGATCCAGAGCTGGAGAAAGAAGCCGAAGGCTCTTA
GGGAGCAGCCAGAGGGCCAAGTGACCAAGAGGATGGGGCTGAGCTGGGGAAGGGGTGGCATCGAGGACCTTCTT
GCATTCTCCTGTGGGAAGCCAGTGCCTTTGCTCCTCTGTCTGCTCTACTCCCACCCCACTACCTCTGGGAA
CCACAGCTCCACAAGGGGGAGAGGCAGCTGGGCCAGACCGAGGTCAAGCCACTCCAAGTCTGCCCTGCCACCC
TCGGCCTCTGTCTTGAAGCCCCACCCCTTTCTCCTGTACATAATGTCACTGGCTTGTGGGATTTTAAATTTA
TCTTCACTCAGCACCAAGGGCCCCGACACTCCACTCCTGCTGCCCCCTGAGCTGAGCAGAGTCATTATTTGAGAG
TTTTGTATTTATTAAACATTTCTTTTTCAGTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

bioRxiv preprint doi: <https://doi.org/10.1101/000000>; this version posted January 1, 2015. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY-NC-ND 4.0 International license.

FIGURE 4

><subunit 1 of 1, 954 aa, 1 stop

><MW: 101960, pI: 8.21, NX(S/T): 5

MPSLPAPPAPLLLLLGLLLLGSRPARGAGPEPPVLPPIRSEKEPLPVRGAAGCTFGGKVYALDE
TWHPDLGQPFQVMRCVLCACEAPQWGRRTGRGPGRVSCKNIKPECPTPACGQPRQLPGHCCQT
CPQERSSSERQPSGLSFEYPRDPEHRSSYSDRGEPGAEERARGDGHTDFVALLTGPRSQAVAR
ARVSLRLRSSLRFSISYRRLDRPTRIRFSDSNGSVLFEHPAAPTQDGLVCGVWRAVPRLSLRL
LRAEQLHVALVTLTHPSGEVWGPLIRHRALAAETFSAILTLEGPPQQGVGGITLLTLSDTED
SLHFLLLFRGLLEPRSGGLTQVPLRLQILHQGQLLRELQANVSAQEPGFAEVLPNLTVQEMD
WLVLGELQMALEWAGRPGLRISGHIAARKSCDVLQSVLCGADALIPVQTGAAGSASLTLLGN
GSLIYQVQVVGTSSEVVAMTLETKPQRDQRTVLCHMAGLQPGGHTAVGICPGLGARGAAML
LQNELFLNVGTDKDFPDGELRGHVAALPYCGHSARHDTLPVPLAGALVLPVKSQAAGHAWLS
LDTHCHLHYEVLLAGLGGSEQGTVAHLLGPPGTPGPRLLKGFYGSEAQGVVKDLEPELLR
HLAKGMASLMITTKGSPRGELRGQVHIANQCEVGGLRLEAAGAEGVRALGAPDTASAAPPVV
PGLPALAPAKPGGPRPRDPNTCFFEGQQRPHGARWAPNYDPLCSLCTCQRRTVICDPVVC
PPSCPHPVQAPDQCCPVCPEKQDVRDLPLPRSRDPGEGCYFDGDRSWRAAGTRWHPVVPF
GLIKCAVCTCKGGTGEVHCEKVQCPRACAQPVVRVNPTDCKQCPVGSQAHPQLGDPMQADG
PRGCRFAGQWFPESQSWHPSVPPFGEMSCITCRGAGVPHCERDDCSLPLSCGSGKESRCCS
RCTAHRPPETRTDPELEKEAEGS

Signal sequence.

amino acids 1-23

N-glycosylation sites.

amino acids 217-221, 351-355, 365-369, 434-438

Tyrosine kinase phosphorylation sites.

amino acids 145-153, 778-786

N-myristoylation sites.

amino acids 20-26, 47-53, 50-56, 69-75, 73-79, 232-238, 236-242,
390-396, 422-428, 473-479, 477-483, 483-489, 489-495, 573-579,
576-582, 580-586, 635-641, 670-676, 773-779, 807-813, 871-877,
905-911

Amidation site.

amino acids 87-91

Cell attachment sequence.

amino acids 165-168

Leucine zipper pattern.

amino acids 315-337

[illegible]

AAGTCA

FIGURE 6

><subunit 1 of 1, 737 aa, 1 stop

><MW: 78475, pI: 5.09, NX(S/T): 11

MQPRRAQAPGAQLLPALALLLLLLGAGPRGSSLANPVPAAPLSAPGPCAAQPCRNGGVCTSR
PEPDPQHPAPAGEPGYSCTCPAGISGANCLVADPCASNPCHHGNCSSSSSSSSSDGYLCICN
EGYEGPNCEQALPSLPATGWTESMAPRQLQVPATQEPDKILPRSQATVTLPTWQPKTGQKV
VEMKWDQVEVIPDIACGNASSNSSAGGRLVSFEVPQNTSVKIRQDATASLILLWKVTATGFQ
QCSLIDGRSVTPLQASGGLVLLLEMLALGNNHFIGFVNDVTKSIVALRLTLVVKVSTCVPG
ESHANDLECSGKGKCTTKPSEATFSCCTCEEQYVGTFCEEYDACQRKPCQNNASCIDANEKQD
GSNFTCVCLPGYTGELCQSKIDYCIDLPCRNGATCISSLSGFTCQCPEGYFGSACEEKVDPC
ASSPCQNNGTCTYVDGVHFTCNCSPGFTGPTCAQLIDFCALSPCAHGTCRSVGTSYKCLCDPG
YHGLYCEEEYNECLSAPCLNAATCRDLVNGYECVCLA EYKGTHCELYKDPCANV SCLNGATC
DSDGLNGTCICAPGFTGEECDIDINECD SNPCHHGGSCLDQPNGYNCHCPHG WVGANCEIHL
QWKS GHMAESLTNMPRHS LYIIIGALCVAFILMLIILIVGICRISRIEYQGSSRPAYEEFY N
CRSIDSEFSNAIASIRHARFGKKSRPAMYDVSP IAYEDYSPDDKPLVTLIKTKDL

Signal sequence.

amino acids 1-28

Transmembrane domain.

amino acids 641-660

N-glycosylation sites.

amino acids 107-111, 204-208, 208-212, 223-227, 286-290, 361-365,
375-379, 442-446, 549-553, 564-568

Glycosaminoglycan attachment site.

amino acids 320-324

Tyrosine kinase phosphorylation sites.

amino acids 490-498, 674-682

N-myristoylation sites.

amino acids 30-36, 56-62, 57-63, 85-91, 106-112, 203-209,
373-379, 449-455, 480-486, 562-568, 565-571

Amidation site.

amino acids 702-706

Aspartic acid and asparagine hydroxylation site.

amino acids 520-532, 596-608

EGF-like domain cysteine pattern signatures.

amino acids 80-92, 121-133, 336-348, 378-390, 416-428, 454-466,
491-503, 529-541, 567-579, 605-617

FIGURE 7

CTCTGGAAGGTCACGGCCACAGGATTCCAACAGTGCTCCCTCATAGATGGACGAAAGTGTGA
CCCCCCTTTCAGGCTTTCAGGGGGACTGGTCCTCCTGGAGGAGATGCTCGCCTTGGGGAATA
ATCACTTTATTGGTTTTGTGAATGATTCTGTGACTAAGTCTATTGTGGCTTTGCGCTTAACT
CTGGTGGTGAAGGTCAGCACCTGTGTGCCGGGGGAGAGTCACGCAAATGACTTGGAGTGTTTC
AGGAAAAGGAAAATGCACCACGAAGCCGTCAGAGGCAACTTTTTTCCTGTACCTGTGAGGAGC
AGTACGTGGGTACTTTCTGTGAAGAATACGATGCTTGCCAGAGGAAACCTTGCCAAAACAAC
GCGAGCTGTATTGATGCAAATGAAAAGCAAGATGGGAGCAATTTACCTGTGTTTGCCTTCC
TGTTTATACTGGAGAGCTTTGCCAACCGAACTGAGATTGGAGCGAACGACCTACACCGAACT
GAGATAGGGGAG

09449 0310 6264660

FIGURE 8

CTCTGGAAGGTCACGGCCACAGGATTCCAACAGTGCTCCCTCATAGATGGACGAAAGTGTGA
CCCCCCTTTCAGGCTTTCAGGGGGACTGGTCCTCCTGGAGGAGATGCTCGCCTTGGGGAATA
ATCACTTTATTGGTTTTGTGAATGATTCTGTGACTAAGTCTATTGTGGCTTTGCGCTTAACT
CTGGTGGTGAAGGTCAGCACCTGTGTGCCGGGGGAGAGTCACGCAAATGACTTGGAGTGTTT
AGGAAAAGGAAAATGCACCACGAAGCCGTCAGAGGCAACTTTTTCTGTACCTGTGAGGAGC
AGTACGTGGGTACTTTCTGTGAAGAATACGATGCTTGCCAGAGGAAACCTTGCCAAAACAAC
GCGAGCTGTATTGATGCAAATGAAAAGCAAGATGGGAGCAATTTACCTGTGTTTGCCTTCC
TGGTTATACTGGAGAGCTTTGCCAACCGAACTGAGATTGGAGCGAACGACCTACACCGAACT
GAGATAGGGGAG

094430 626460

FIGURE 9

GCTGAGTCTGCTGCTCCTGCTGCTGCTGCTCCAGCCTGTAACCTGTGCCTACACCACGCCAG
GCCCCCCCAGAGCCCTCACCACGCTGGGCGCCCCAGAGCCCACACCATGCCGGGCACCTAC
GCTCCCTCGACCACACTCAGTAGTCCCAGCACCCAGGGCCTGCAAGAGCAGGCACGGGCCCT
GATGCGGGACTTCCCGCTCGTGGACGGCCACAACGACCTGCCCCTGGTCCTAAGGCAGGTTT
ACCAGAAAGGGCTACAGGATGTTAACCTGCGCAATTTTCAGCTACGGCCAGACCAGCCTGGAC
AGGCTTAGAGATGGCCTCGTGGGCGCCAGTTCTGGTCAGCCTATGTGCCATGCCAGACCCA
GGACCGGGATGCCCTGCGCCTCACCTGGAGCAGATTGACCTCATA CGCCGCATGTGTGCCT
CCTATTCTGAGCTGGAGCTTGTGACCTCGGCTAAAGCTCTGAACGACACTCAGAAATTGGCC
TGCCTCATCGGTGTAGAGGGTGGCCACTCGCTGGACAATAGCCTCTCCATCTTACGTACCTT
CTACATGCTGGGAGTGCGCTACCTGACGCTCACCCACACCTGCAACACACCCTGGGCAGAGA
GCTCCGCTAAGGGCGTCCACTCCTTCTACAACAACATCAGCGGGCTGACTGACTTTGGTGAG
AAGGTGGTGGCAGAAATGAACCGCCTGGGCATGATGGTAGACTTATCCCATGTCTCAGATGC
TGTGGCACGGCGGGCCCTGGAAGTGTACAGGCACCTGTGATCTTCTCCCACTCGGCTGCCC
GGGGTGTGTGCAACAGTGCTCGGAATGTTCTGATGACATCCTGCAGCTTCTGAAGAAGAAC
GGTGGCGTCGTGATGGTGTCTTTGTCCATGGGAGTAATACAGTGCAACCCATCAGCCAATGT
GTCCACTGTGGCAGATCACTTCGACCACATCAAGGCTGTCAATTGGATCCAAGTTCATCGGGA
TTGGTGGAGATTATGATGGGGCCGGCAAATTCCTCAGGGGCTGGAAGACGTGTCCACATAC
CCGGTCCTGATAGAGGAGTTGCTGAGTCGTGGCTGGAGTGAGGAAGAGCTTCAGGGTGTCTT
TCGTGGAAACCTGCTGCGGGTCTTCAGACAAGTGGAAAAGGTACAGGAAGAAAACAAATGGC
AAAGCCCCCTTGAGGACAAGTTCCCGGATGAGCAGCTGAGCAGTTCTTGCCACTCCGACCTC
TCACGTCTGCGTCAGAGACAGAGTCTGACTTCAGGCCAGGAACTCACTGAGATTCCCATACA
CTGGACAGCCAAGTTACCAGCCAAGTGGTCAGTCTCAGAGTCCTCCCCCACATGGCCCCAG
TCCTTGACAGTTGTGGCCACCTTCCCAGTCCTTATTCTGTGGCTCTGATGACCCAGTTAGTCC
TGCCAGATGTCACTGTAGCAAGCCACAGACACCCACAAAGTTCCCCTGTTGTGCAGGCACA
AATATTTCTGAAATAAATGTTTTGGACATAG

[illegible]

```
<subunit 1 of 1, 433 aa, 1 stop
```

MPGTYAPSTTLSSPSTQGLQEQRALMRDFPLVDGHNDLPLVLRQVYQKGLQDVNLRNFSYG
QTSLDRLRDGLVGAQFWSAYVPCQTQDRDALRLTLEQIDLIIRMCASYSELELVTSAKALND
TQKLACLI GVEGGHSLDNSLSILRTFYMLGVRYLTLTHTCNTPWAESSAKGVHSFYNNISGL
TDFGEKVVAEMNRLGMMVDLSHVSDAVARRALEVSQAPVIFSHSAARGVCNSARNVPDDILQ
LLKKNGGVVMVSLSMGVIQCNPSANVSTVADHFDHIKAVIGSKFIGIGGDYDGAGKFPQGLE
DVSTYPVLI EELLSRGWSEEELQGVLRGNLLRVFRQVEKVQEEKWQSPLEDKFPDEQLSSS
CHSDLSRLRQRQSLTSGQELTEIPIHWTAKLPKWSVSESSPHMAPVLAVVATFPVLILWL

amino acids 58-62, 123-127, 182-186, 273-277

amino acids 72-78, 133-139, 234-240, 264-270, 334-340, 389-395

amino acids 134-157

FIGURE 11

AAAACCTATAAATATTCCGGATTATTCATACCGTCCCACCATCGGGCGCGGATCCGCGGCCG
CGAATTCTAAACCAACATGCCGGGCACCTACGCTCCCTCGACCACACTCAGTAGTCCCAGCA
CCCAGGGCCTGCAAGAGCAGGCACGGGGCCCTGATGCGGGACTTCCCGCTCGTGGACGGCCAC
AACGACCTGCCCCCTGGTCCTAAGGCAGGTTTACCAGAAAGGGCTACAGGATGTTAACCTGCG
CAATTTTCAGCTACGGCCAGACCAGCCTGGACAGGCTTAGAGATGGCCTCGTGGGCGCCCAGT
TCTGGTCAGCCTATGTGCCATGCCAGACCCAGGACCGGGATGCCCTGCGCCTCACCTGGAG
CAGATTGACCTCATACGCCGCATGTGTGCCTCCTATTCTGAGCTGGAGCTTGTGACCTCGGC
TAAAGCTCTGAACGACACTCAGAAATTGGCCTGCCTCATCGGTGTAGAGGGTGGCCACTCGC
TGGACAATAGCCTCTCCATCTTACGTACCTTCTACATGCTGGGAGTGCGCTACCTGACGCTC
ACCCACACCTGCAACACACCCTGGGCAGAGAGCTCCGCTAAGGGCGTCCACTCCTTCTACAA
CAACATCAGCGGGCTGACTGACTTTGGTGAGAAGGTGGTGGCAGAAATGAACCGCCTGGGCA
TGATGGTAGACTTATCCCATGTCTCAGATGCTGTGGCACGGCGGGCCCTGGAAAGTGTACAG
GCACCTGTGATCTTCTCCCACTCGGCTGCCCCGGGTGTGTGCAACAGTGCTCGGAATGTTCC
TGATGACATCCTGCAGCTTCTGAAGAAGAACGGTGGCGTCGTGATGGTGTCTTTGTCCATGG
GAGTAATACAGTGCAACCCATCAGCCAATGTGTCCACTGTGGCAGATCACTTCGACCACATC
AAGGCTGTCATTGGATCCAAGTTCATCGGGATTGGTGGAGATTATGATGGGGCCGGCAAATT
CCCTCAGGGGCTGGAAGACGTGTCCACATACCCGGTCCTGATAGAGGAGTTGCTGAGTCGTG
GCTGGAGTGAGGAAGAGCTTCAGGGTGTCTTCGTGGAAACCTGCTGCGGGTCTTCAGACAA
GTGGAAAAGGTACAGGAAGAAAACAAATGGCAAAGCCCCTTGGAGGACAAGTTCCCGGATGA
GCAGCTGAGCAGTTCCTGCCACTCCGACCTCTCACGTCTGCGTCAGAGACAGAGTCTGACTT
CAGGCCAGGAACTCACTGAGATTCCCATACTGGACAGCCAAGTTACCAGCCAAGTGGTCA
GTCTCAGAGTCCTCCCCCACCCTGACAAAACCTCACACATGCCACCGTGCCACGACCTGA
ACTCCTGGGGGGACCGTCAGTCTTCTCTTCCCCCAAACCCAAGGACACC

FIGURE 12

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA35872

><subunit 1 of 1, 446 aa, 0 stop

><NX(S/T): 5

MPGTYAPSTTLSSPSTQGLQEQARALMRDFPLVDGHNDLPLVLRQVYQKGLQDVNLRNFSYG
QTSLDRLRDGLVGAQFWSAYVPCQTQDRDALRLTLEQIDLIIRMCASYSELELVTSAKALND
TQKLACLIGVEGGHSLDNSLSILRTFYMLGVRYLTLTHTCNTPWAESSAKGVHSFYNNISGL
TDFGEKVVAEMNRLGMMVDLSHVSDAVARRALEVSQAPVIFSHSAARGVCNSARNVPDDILQ
LLKKNGGVVMVSLSMGVIQCNPSANVSTVADHFDHIKAVIGSKFIGIGGDYDGAGKFPQGLE
DVSTYPVLIEELLSRGWSEEELQGVLRGNLLRVFRQVEKVQEENKWQSPLDKFPDEQLSSS
CHSDLSRLRQRQSLTSGQELTEIP IHWTAKLPAKWSVSESSPHDPKTHTCPPCPAPELLGGP
SVFLFPPKPKDT

TEEO" 6264660

FIGURE 13

CGCCCAGCGACGTGCGGGCGGCCTGGCCCCGCGCCCTCCCGCGCCCGGCCTGCGTCCCGCGCC
CTGCGCCACCGCCGCGGAGCCGCAGCCCGCGCGCGCCCCCGGCAGCGCCGGCCCCATGCCCC
GCCGGCCGCGGGGCCCCGCGCCCAATCCGCGCGGCGGCCGCGCCGTTGCTGCCCCCTGCT
GCTGCTGCTCTGCGTCCTCGGGGCGCCGCGAGCCGGATCAGGAGCCCACACAGCTGTGATCA
GTCCCCAGGATCCCACGCTTCTCATCGGCTCCTCCCTGCTGGCCACCTGCTCAGTGCACGGA
GACCCACCAGGAGCCACCGCCGAGGGCCTCTACTGGACCCTCAACGGGCGCCGCTGCCCCC
TGAGCTCTCCCGTGTACTCAACGCCTCCACCTTGGCTCTGGCCCTGGCCAACCTCAATGGGT
CCAGGCAGCGGTGCGGGGACAACCTCGTGTGCCACGCCCCGTGACGGCAGCATCCTGGCTGGC
TCCTGCCTCTATGTTGGCCTGCCCCCAGAGAAACCCGTCAACATCAGCTGCTGGTCCAAGAA
CATGAAGGACTTGACCTGCCGCTGGACGCCAGGGGCCCCACGGGGAGACCTTCCTCCACACCA
ACTACTCCCTCAAGTACAAGCTTAGGTGGTATGGCCAGGACAACACATGTGAGGAGTACCAC
ACAGTGGGGCCCCACTCCTGCCACATCCCCAAGGACCTGGCTCTCTTTACGCCCTATGAGAT
CTGGGTGGAGGCCACCAACCGCCTGGGCTCTGCCCCGCTCCGATGTACTCACGCTGGATATCC
TGGATGTGGTGACCACGGACCCCCCGCCCGACGTGCACGTGAGCCGCGTCGGGGGCTGGAG
GACCAGCTGAGCGTGCGCTGGGTGTGCGCACCCGCCCTCAAGGATTCCTCTTTCAAGCCAA
ATACCAGATCCGCTACCGAGTGAGGACAGTGTGGAAGGTGGTGACGATGTGAGCA
ACCAGACCTCCTGCCGCTGGCCGGCCTGAAACCCGGCACCGTGTACTTCGTGCAAGTGCGC
TGCAACCCCTTTGGCATCTATGGCTCCAAGAAAGCCGGGATCTGGAGTGAGTGAGCCACCC
CACAGCCGCCTCCACTCCCCGCAGTGAGCGCCCCGGGCCCCGGGCGGCGGGGCGTGCGAACCGC
GGGGCGGAGAGCCGAGCTCGGGGCGGTGCGGCGCGAGCTCAAGCAGTTCCTGGGCTGGCTC
AAGAAGCACGCGTACTGCTCCAACCTCAGCTTCCGCCTCTACGACCAGTGGCGAGCCTGGAT
GCAGAAGTCGCACAAGACCCGCAACCAGGACGAGGGGATCCTGCCCTCGGGCAGACGGGGCA
CGGCGAGAGGTCCTGCCAGATAAGCTGTAGGGGCTCAGGCCACCCTCCCTGCCACGTGGAGA
CGCAGAGGCCGAACCCAAACTGGGGCCACCTCTGTACCTCACTTCAGGGCACCTGAGCCAC
CCTCAGCAGGAGCTGGGGTGGCCCCCTGAGCTCCAACGGCCATAACAGCTCTGACTCCCACGT
GAGGCCACCTTTGGGTGCACCCAGTGGGTGTGTGTGTGTGTGTGAGGGTTGGTTGAGTTGC
CTAGAACCCCTGCCAGGGCTGGGGGTGAGAAGGGGAGTCATTACTCCCCATTACCTAGGGCC
CCTCCAAAAGAGTCCTTTTAAATAAATGAGCTATTTAGGTGCTGTGATTGTGAAAAAAAAA
AA

[illegible]

MPAGRRGPAAQSARRPPPLLPLLLLLL CVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATCSV
HGDPPGATAEGLYWTLNGRRLPPELSRVLNASTLALALANLNGSRQSRGDNLVCHARDGSIL
AGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSKYKLRWYGQDNTCEE
YHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPDVHVS RVGG
LEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVDDVSNQTS CRLAGLKPGTVYFVQ
VRCNPFGIYGSKKAGI WSEWSHPTAASTPRSERPGPGGGACEPRGGEPSSGPVRRELKQFLG
WLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQDEGILPSGRRGTARGPAR

amino acids 1-30

amino acids 44-61

amino acids 92-96, 104-108, 140-144, 168-172, 292-296, 382-386

amino acids 413-417

amino acids 30-36, 37-43, 73-79, 121-127, 179-185, 218-224,
300-306, 317-323, 320-326, 347-353, 355-361, 407-413

amino acids 3-7, 79-83, 411-415

amino acids 325-331

FIGURE 15

CCCACGCGTCCGCTGGTGTAGATCGAGCAACCCTCTAAAAGCAGTTTAGAGTGGTAAAAAA
AAAAAAAACACACCAAACGCTCGCAGCCACAAAAGGGATGAAATTTCTTCTGGACATCCTC
CTGCTTCTCCCGTTACTGATCGTCTGCTCCCTAGAGTCCTTCGTGAAGCTTTTTATTCTTAA
GAGGAGAAAATCAGTCACCGGCGAAATCGTGCTGATTACAGGAGCTGGGCATGGAATTGGGA
GACTGACTGCCTATGAATTTGCTAAACTTAAAAGCAAGCTGGTTCTCTGGGATATAAATAAG
CATGGACTGGAGGAAACAGCTGCCAAATGCAAGGGACTGGGTGCCAAGGTTTATACCTTTGT
GGTAGACTGCAGCAACCGAGAAGATATTTACAGCTCTGCAAAGAAGGTGAAGGCAGAAATTG
GAGATGTTAGTATTTTAGTAAATAATGCTGGTGTAGTCTATACATCAGATTTGTTTGCTACA
CAAGATCCTCAGATTGAAAAGACTTTTGAAGTTAATGTACTTGACATTTCTGGACTACAAA
GGCATTCTTCTTCTGCAATGACGAAGAATAACCATGGCCATATTGTCACTGTGGCTTCGGCAG
CTGGACATGTCTCGGTCCCCTTCTTACTGGCTTACTGTTCAAGCAAGTTTGCTGCTGTTGGA
TTTCATAAACTTTGACAGATGAACTGGCTGCCTTACAAATAACTGGAGTCAAAACAACATG
TCTGTGTCCTAATTTGTAACACTGGCTTCATCAAAAATCCAAGTACAAGTTTGGGACCCA
CTCTGGAACCTGAGGAAGTGGTAAACAGGCTGATGCATGGGATTCTGACTGAGCAGAAGATG
ATTTTTATTCCATCTTCTATAGCTTTTTTAACAACATTGGAAAGGATCCTTCTGAGCGTTT
CCTGGCAGTTTTAAAACGAAAAATCAGTGTTAAGTTTGATGCAGTTATTGGATATAAAATGA
AAGCGCAATAAGCACCTAGTTTTCTGAAAACCTGATTTACCAGGTTTAGGTTGATGTCATCTA
ATAGTGCCAGAATTTAATGTTTGAACCTCTGTTTTTTCTAATTATCCCCATTTCTTCAATA
TCATTTTTGAGGCTTTGGCAGTCTTCATTTACTACCACTTGTTCTTTAGCCAAAAGCTGATT
ACATATGATATAAACAGAGAAATACCTTTAGAGGTGACTTTAAGGAAAATGAAGAAAAAGAA
CCAAAATGACTTTATTAAAATAATTTCCAAGATTATTTGTGGCTCACCTGAAGGCTTTGCAA
AATTGTACCATAACCGTTTATTTAACATATATTTTTATTTTTGATTGCACTTAAATTTGT
ATAATTTGTGTTTCTTTTTCTGTTCTACATAAAATCAGAACTTCAAGCTCTCTAAATAAAA
TGAAGGACTATATCTAGTGGTATTTTACAATGAATATCATGAACTCTCAATGGGTAGGTTTC
ATCCTACCCATTGCCACTCTGTTTCCTGAGAGATACCTCACATTCCAATGCCAAACATTTCT
GCACAGGGAAGCTAGAGGTGGATACACGTGTTGCAAGTATAAAAGCATCACTGGGATTTAAG
GAGAATTGAGAGAATGTACCCACAAATGGCAGCAATAATAAATGGATCACACTTAAAAAAA
AA
AA

FIGURE 16

</usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA34436

<subunit 1 of 1, 300 aa, 1 stop

<MW: 32964, pI: 9.52, NX(S/T): 1

MKFLLDILLLLPLLIIVCSLESFVKLFIPKRRKSVTGEIVLITGAGHGIGRLTAYEFAKLKSK
LVLWDINKHGLEETAACKCKGLGAKVHTFVVDCSNREDIYSSAKKVKAIEIGDVSILVNNAGVV
YTSDLFATQDPQIEKTFEVNVLAHFWTTKAFLPAMTKNNHGHIVTVASAAGHVSVFPFLLAYC
SSKFAAVGFHKTLTDELAALQITGVKTTCLCPNFVNTGFIKNPSTSLGPTLEPEEVNRLMH
GILTEQKMIFIPSSIAFLTTLERILPERFLAVLKRKISVKFDAVIGYKMQAQ

Signal sequence.

amino acids 1-19

Transmembrane domain.

amino acids 170-187

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 30-34, 283-287

N-myristoylation sites.

amino acids 43-49, 72-78, 122-128, 210-216

107630 6264660

FIGURE 17

GACTAGTTCTCTTGGAGTCTGGGAGGAGGAAAGCGGAGCCGGCAGGGAGCGAACCAGGACTG
GGGTGACGGCAGGGCAGGGGGCGCCTGGCCGGGGAGAAGCGCGGGGGCTGGAGCACCAACAA
CTGGAGGGTCCGGAGTAGCGAGCGCCCCGAAGGAGGCCATCGGGGAGCCGGGAGGGGGGACT
GCGAGAGGACCCCGGCGTCCGGGGCTCCCGGTGCCAGCGCTATGAGGCCACTCCTCGTCCTGC
TGCTCCTGGGCCTGGCGGCCGGCTCGCCCCACTGGACGACAACAAGATCCCCAGCCTCTGC
CCGGGGCACCCCGGCCTTCCAGGCACGCCGGGGCCACCATGGCAGCCAGGGCTTGCCGGGGCCG
CGATGGCCGCGACGGCCGCGACGGCGCGCCCCGGGGCTCCGGGAGAGAAAGGCGAGGGCGGGA
GGCCGGGACTGCCGGGACCTCGAGGGGACCCCGGGCCGCGAGGAGAGGCGGGACCCGCGGGG
CCCACCGGGCCTGCCGGGGAGTGCTCGGTGCCTCCGCGATCCGCCTTCAGCGCCAAGCGCTC
CGAGAGCCGGGTGCCTCCGCCGTCTGACGCACCCTTGCCCTTCGACCGCGTGCTGGTGAACG
AGCAGGGACATTACGACGCCGTACCCGGCAAGTTACCTGCCAGGTGCCTGGGGTCTACTAC
TTCGCCGTCCATGCCACCGTCTACCGGGCCAGCCTGCAGTTTGATCTGGTGAAGAATGGCGA
ATCCATTGCCTCTTTCTTCCAGTTTTTCGGGGGGTGGCCCAAGCCAGCCTCGCTCTCGGGGG
GGGCCATGGTGAGGCTGGAGCCTGAGGACCAAGTGTGGGTGCAGGTGGGTGTGGGTGACTAC
ATTGGCATCTATGCCAGCATCAAGACAGACAGCACCTTCTCCGGATTTCTGGTGTACTCCGA
CTGGCACAGCTCCCCAGTCTTTGCTTAGTGCCCACTGCAAAGTGAGCTCATGCTCTCACTCC
TAGAAGGAGGGTGTGAGGCTGACAACCAGGTCATCCAGGAGGGCTGGCCCCCTGGAATATT
GTGAATGACTAGGGAGGTGGGGTAGAGCACTCTCCGTCCTGCTGCTGGCAAGGAATGGGAAC
AGTGGCTGTCTGCGATCAGGTCTGGCAGCATGGGGCAGTGGCTGGATTTCTGCCCAAGACCA
GAGGAGTGTGCTGTGCTGGCAAGTGTAAGTCCCCAGTTGCTCTGGTCCAGGAGCCCACGGT
GGGGTGCTCTCTTCTGGTCTCTGCTTCTCTGGATCCTCCCCACCCCTCCTGCTCCTGGG
GCCGGCCCTTTTCTCAGAGATCACTCAATAAACCTAAGAACCCTCATAAAAAAAAAAAAAA
AAAAAAAAAAAAA

FIGURE 18

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA40592

><subunit 1 of 1, 243 aa, 1 stop

><MW: 25298, pI: 6.44, NX(S/T): 0

MRPLLVLALLGLAAGSPPLDDNKIPSLCPGHPGLPGTPGHHGSQGLPGRDGRDGRDGAPGAP
GEKGEGGRPGLPGPRGDPGPRGEAGPAGPTGPAGECSVPPRSAFSAKRSESRVPPPSDAPLP
FDRVLVNEQGHYDAVTGKFTCQVPGVYYFAVHATVYRASLQFDLVKNGESIASFFQFFGGWP
KPASLSGGAMVRLEPEDQVWVQVGVDYIGIYASIKTDSTFSGFLVYSDWHSSPVFA

Signal sequence.

amino acids 1-15

N-myristoylation sites.

amino acids 11-17, 68-74, 216-222

Cell attachment sequence.

amino acids 77-80

FOR "6264469"

FIGURE 19

CTCTTTTGTCCACCAGCCCAGCCTGACTCCTGGAGATTGTGAATAGCTCCATCCAGCCTGAG
AAACAAGCCGGGTGGCTGAGCCAGGCTGTGCACGGAGCACCTGACGGGCCCAACAGACCCAT
GCTGCATCCAGAGACCTCCCCTGGCCGGGGGCATCTCCTGGCTGTGCTCCTGGCCCTCCTTG
GCACCACCTGGGCAGAGGTGTGGCCACCCCAGCTGCAGGAGCAGGCTCCGATGGCCGGAGCC
CTGAACAGGAAGGAGAGTTTCTTGCTCCTCTCCCTGCACAACCGCCTGCGCAGCTGGGTCCA
GCCCCCTGCGGCTGACATGCGGAGGCTGGACTGGAGTGACAGCCTGGCCCAACTGGCTCAAG
CCAGGGCAGCCCTCTGTGGAATCCCAACCCCGAGCCTGGCATCCGGCCTGTGGCGCACCCCTG
CAAGTGGGCTGGAACATGCAGCTGCTGCCCCGCGGGCTTGGCGTCCTTTGTTGAAGTGGTCAG
CCTATGGTTTTGCAGAGGGGCAGCGGTACAGCCACGCGGCAGGAGAGTGTGCTCGCAACGCCA
CCTGCACCCACTACACGCAGCTCGTGTGGGCCACCTCAAGCCAGCTGGGCTGTGGGCGGCAC
CTGTGCTCTGCAGGCCAGACAGCGATAGAAGCCTTTGTCTGTGCCTACTCCCCGGAGGCAA
CTGGGAGGTCAACGGGAAGACAATCATCCCCTATAAGAAGGGTGCCTGGTGTTCGCTCTGCA
CAGCCAGTGTCTCAGGCTGCTTCAAAGCCTGGGACCATGCAGGGGGGCTCTGTGAGGTCCCC
AGGAATCCTTGTGCGATGAGCTGCCAGAACCATGGACGTCTAACATCAGCACCTGCCACTG
CCACTGTCCCCCTGGCTACACGGGCAGATACTGCCAAGTGAGGTGCAGCCTGCAGTGTGTGC
ACGGCCGGTTCCGGGAGGAGGAGTGCTCGTGCCTGTGTGACATCGGCTACGGGGGAGCCCAG
TGTGCCACCAAGGTGCATTTTCCCTTCCACACCTGTGACCTGAGGATCGACGGAGACTGCTT
CATGGTGTCTTCAGAGGCAGACACCTATTACAGAGCCAGGATGAAATGTCAGAGGAAAGGCG
GGGTGCTGGCCCAGATCAAGAGCCAGAAAGTGACAGGACATCCTCGCCTTCTATCTGGGCCGC
CTGGAGACCACCAACGAGGTGACTGACAGTGACTTCGAGACCAGGAACTTCTGGATCGGGCT
CACCTACAAGACCGCCAAGGACTCCTTCCGCTGGGCCACAGGGGAGCACCAGGCCTTCACCA
GTTTTGCCTTTGGGCAGCCTGACAACCACGGGCTGGTGTGGCTGAGTGCTGCCATGGGGTTT
GGCAACTGCGTGGAGCTGCAGGCTTCAGCTGCCTTCAACTGGAACGACCAGCGCTGAAAAC
CCGAAACCGTTACATCTGCCAGTTTGGCCAGGAGCACATCTCCCGGTGGGGCCCAGGGTCCT
GAGGCCTGACCACATGGCTCCCTCGCCTGCCCTGGGAGCACCGGCTCTGCTTACCTGTCTGC
CCACCTGTCTGGAACAAGGGCCAGGTAAAGACCACATGCCTCATGTCCAAAGAGGTCTCAGA
CCTTGACAATGCCAGAAGTTGGGCAGAGAGAGGCAGGGAGGCCAGTGAGGGCCAGGGAGTG
AGTGTTAGAAGAAGCTGGGGCCCTTCGCCTGCTTTTGATTGGGAAGATGGGCTTCAATTAGA
TGGCGAAGGAGAGGACACCGCCAGTGGTCCAAAAAGGCTGCTCTCTTCCACCTGGCCCAGAC
CCTGTGGGGCAGCGGAGCTTCCCTGTGGCATGAACCCACGGGGTATTAAATTATGAATCAG
CTGAAAAAAAAAAAAA

09499-183101

FIGURE 20

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44176

<subunit 1 of 1, 455 aa, 1 stop

<MW: 50478, pI: 8.44, NX(S/T): 2

MLHPETSPGRGHLLAVLLALLGTTWAEVWPPQLQEAPMAGALNRKESFLLLSLHNRLRSWV
QPPAADMRRLDWSDSLAQLAQARAALCGIPTPSLASGLWRTLQVGWNMQLLPAGLASFVEVV
SLWFAEGQRYSHAAGECARNATCTHYTQLVWATSSQLGCGRHLCSAGQTAIEAFVCAYSPGG
NWEVNGKTIIPYKKGAWCSLCTASVSGCFKAWDHAGGLCEVPRNPCRMSCQNHGRLNISTCH
CHCPPGYTGRYCQVRCSLQCVHGRFREEECSCVCDIGYGGAQCATKVHFPFHTCDLRIDGDC
FMVSSEADTYRARMKCQRKGGVLAQIKSQKVQDILAFYLGRLETTNEVTDSDFETRNFwig
LTYKTAKDSFRWATGEHQAFTSFAFGQPDNHGLVWLSAAMGFGNCVELQASAAFNWNDQRCK
TRNRYICQFAQEHISRWGPGS

Signal sequence.

amino acids 1-26

Transmembrane domain.

amino acids 110-124

N-glycosylation sites.

amino acids 144-148, 243-247

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 45-49

N-myristoylation sites.

amino acids 22-28, 99-105, 131-137, 201-207, 213-219, 287-293,
288-294, 331-337, 398-404

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 204-215

EGF-like domain cysteine pattern signature.

amino acids 249-261, 280-292

C-type lectin domain signature.

amino acids 417-442

NOTED "52644650

FIGURE 21

CGGACGCGTGGGCTGGGCGCTGCAAAGCGTGTCCCGCCGGGTCCCCGAGCGTCCCGCGCCCT
CGCCCCGCC**ATG**CTCCTGCTGCTGGGGCTGTGCCTGGGGCTGTCCCTGTGTGTGGGGTCGCA
GGAAGAGGCGCAGAGCTGGGGCCACTCTTCGGAGCAGGATGGACTCAGGGTCCCGAGGCAAG
TCAGACTGTTGCAGAGGCTGAAAACCAAACCTTTGATGACAGAATTCTCAGTGAAGTCTACC
ATCATTTCCTGTTATGCCTTCACTACGGTTTCTGCGAGAATGCTGAACAGAGCTTCTGAAGA
CCAGGACATTGAGTTCAGATGCAGATTCCAGCTGCAGCTTTCATCACCAACTTCACTATGC
TTATTGGAGACAAGGTGTATCAGGGCGAAATTACAGAGAGAGAAAAGAAGAGTGGTGATAGG
GTAAAAGAGAAAAGGAATAAAACACAGAAGAAAATGGAGAGAAGGGGACTGAAATATTCAG
AGCTTCTGCAGTGATTCCCAGCAAGGACAAAGCCGCCTTTTTCTGAGTTATGAGGAGCTTC
TGCAGAGGCGCTGGGCAAGTACGAGCACAGCATCAGCGTGC GGCCCCAGCAGCTGTCCGGG
AGGCTGAGCGTGGACGTGAATATCCTGGAGAGCGCGGGCATCGCATCCCTGGAGGTGCTGCC
GCTTCACAACAGCAGGCAGAGGGGAGTGGGCGCGGGGAAGATGATTCTGGGCCTCCCCCAT
CTACTGTCATTAAACCAAATGAAACATTTGCCAACATAATTTTTAAACCTACTGTAGTACAA
CAAGCCAGGATTGCCCAGAATGGAATTTTGGGAGACTTTATCATTAGATATGACGTCAATAG
AGAACAGAGCATTGGGGACATCCAGGTTCTAAATGGCTATTTTGTGCACTACTTTGCTCCTA
AAGACCTTCCTCCTTTACCCAAGAATGTGGTATTTCGTGCTTGACAGCAGTGCTTCTATGGTG
GGAACCAAACCTCCGGCAGACCAAGGATGCCCTCTTCACAATTCCTCATGACCTCCGACCCCA
GGACCGTTTCAGTATCATTGGATTTTCCAACCGGATCAAAGTATGGAAGGACCACTTGATAT
CAGTCACTCCAGACAGCATCAGGGATGGGAAAGTGACATTCAACCATATGTCACCCACTGGA
GGCACAGACATCAACGGGGCCCTGCAGAGGGCCATCAGGCTCCTCAACAAGTACGTGGCCCA
CAGTGGCATTGGAGACCGGAGCGTGTCCCTCATCGTCTTCTGACGGATGGGAAGCCACGG
TCGGGGAGACGCACACCCTCAAGATCCTCAACAACACCCGAGAGGCCGCCGAGGCCAAGTC
TGCATCTTCACCATTTGGCATCGGCAACGACGTGGACTTCAGGCTGCTGGAGAACTGTCGCT
GGAGAACTGTGGCCTCACACGGCGCGTGCACGAGGAGGAGGACGCAGGCTCGCAGCTCATCG
GGTTCTACGATGAAATCAGGACCCCGCTCCTCTCTGACATCCGCATCGATTATCCCCCAGC
TCAGTGGTGCAGGCCACCAAGACCCGTGTTCCCCAACTACTTCAACGGCTCGGAGATCATCAT
TGCGGGGAAGCTGGTGGACAGGAAGCTGGATCACCTGCACGTGGAGGTCAACGCCAGCAACA
GTAAGAAATTCATCATCCTGAAGACAGATGTGCCTGTGCGGCCTCAGAAGGCAGGGAAAGAT
GTCACAGGAAGCCCCAGGCCTGGAGGCGATGGAGAGGGGGACACCAACCACATCGAGCGTCT
CTGGAGCTACCTCACCACAAAGGAGCTGCTGAGCTCCTGGCTGCAAAGTGACGATGAACCGG
AGAAGGAGCGGCTGCGGCAGCGGGCCAGGCCCTGGCTGTGAGCTACCGCTTCCTCACTCCC
TTCACCTCCATGAAGCTGAGGGGGCCGGTCCCACGCATGGATGGCCTGGAGGAGGCCACGG
CATGTCGGCTGCCATGGGACCCGAACCGGTGGTGCAGAGCGTGCAGGAGCTGGCACGCAGC
CAGGACCTTTGCTCAAGAAGCCAAACTCCGTCAAAAAAAAAACAAAACAAAAAAGAA
CATGGGAGAGATGGTGTTTTTCTCTCCACCACCTGGGGATACGAT**TGA**GGAAGATGGCCACCT
GCAAGCCAGGAAGACGGCCCTCACCAGACACCATGTCTGCTGGCACCTTGATCTTGACCTC
CCAGCCTCCAGAACTGTGAGAAATAAATGTGTTTTGTTTAAGCTAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 22

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44192

<subunit 1 of 1, 694 aa, 1 stop

<MW: 77400, pI: 9.54, NX(S/T): 6

MLLLLGLCLGLSLCVGSQEEAQSWGHSSEQDGLRVPRQVRLQLKTKPLMTEFSVKSTIIS
RYAFTTVSCRMLNRRASEDQDIEFQMQIPAAAFITNFTMLIGDKVYQGEITEREKKSGDRVKE
KRNKTTEENGEKGTEIFRASAVIPSKDKAAFFLSYEELLQRRLGKYEHSISVRPQQLSGRLS
VDVNILESAGIASLEVLPLHNSRQRGSGRGEDDSGPPPSTVINQNETFANIIFKPTVVQQAR
IAQNGILGDFIIRYDVNREQSIGDIQVLNGYFVHYFAPKDLPLPKNVVFLDSSASMVGTK
LRQTKDALFTILHDLRPQDRFSIIIGFSNRIKVWKDHLISVTPDSIRDGKVYIHHMSPTGGTD
INGALQRAIRLLNKYVAHSGIGDRSVSLIVFLTDGKPTVGETHTLKILNNTREAARGQVCIF
TIGIGNDVDFRLLEKLSLENCGLTRRVHEEEDAGSQLIGFYDEIRTPLLSDIRIDYPPSSVV
QATKTLFPNYFNGSEII IAGKLVDRKLDHLHVEVTASNSKKFII LKTDVPVRPQKAGKDVTC
SPRPGGDGEGDTNHIERLWSYLTTKELLSSWLQSDDEPEKERLRQRAQALAVSYRFLTPFTS
MKLRGPVPRMDGLEEAHGMSAAMGPEPVVQSVRGAGTQPGPLLKKPNSVKKKQNKTKKRHGR
DGVFPLHHLGIR

Signal sequence.

amino acids 1-14

N-glycosylation sites.

amino acids 97-101, 127-131, 231-235, 421-425, 508-512, 674-678

Glycosaminoglycan attachment sites.

amino acids 213-217, 391-395

N-myristoylation sites.

amino acids 6-12, 10-16, 212-218, 370-376, 632-638, 638-644

054459-03101
TOTAL 624459

[illegible]

CGGACGCGTGGGGTGCCCGACATGGCGAGTGTAGTGTCTGCCGAGCGGATCCCAGTGTGCGGC
GGCAGCGGCGGCGGCGGCCTCCCCGGGCTCCGGCTTCTGCTGTTGCTCTTCTCCGCCGCGG
CACTGATCCCCACAGGTGATGGGCAGAATCTGTTTACGAAAGACGTGACAGTGATCGAGGGA
GAGGTTGCGACCATCAGTTGCCAAGTCAATAAGAGTGACGACTCTGTGATTCTAGCTACTGAA
TCCCAACAGGCAGACCATTTATTTTCAGGGACTTCAGGCCTTTGAAGGACAGCAGGTTTTAGT
TGCTGAATTTTTCTAGCAGTGAACCTCAAAGTATCATTGACAAACGTCTCAATTTCTGATGAA
GGAAGATACTTTTGCCAGCTCTATACCGATCCCCCACAGGAAAGTTACACCACCATCACAGT
CCTGGTCCCACCACGTAATCTGATGATCGATATCCAGAAAGACACTGCGGTGGAAGGTGAGG
AGATTGAAGTCAACTGCACTGCTATGGCCAGCAAGCCAGCCACGACTATCAGGTGGTTCAA
GGGAACACAGAGCTAAAAGGCAAATCGGAGGTGGAAGAGTGGTCAGACATGTAACTGTGAC
CAGTCAGCTGATGCTGAAGGTGCACAAGGAGGACGATGGGGTCCCAGTGATCTGCCAGGTGG
AGCACCTGCGGTCACTGGAAACCTGCAGACCCAGCGGTATCTAGAAGTACAGTATAAGCCT
CAAGTGACATTCAGATGACTTATCCTCTACAAGGCTTAACCCGGAAGGGGACGCGCTTGA
GTTAACATGTGAAGCCATCGGGAAGCCCCAGCCTGTGATGGTAACTTGGGTGAGAGTCGATG
ATGAAATGCCTCAACACGCCGTACTGTCTGGGCCCCAACCTGTTTCATCAATAACCTAAACAA
ACAGATAATGGTACATACCGCTGTGAAGCTTCAAACATAGTGGGGAAAGCTCACTCGGATTA
TATGCTGTATGTATACGATCCCCCACAACTATCCCTCCTCCACAACAACCACCACCACCA
CCACCACCACCACCACCACCATCCTTACCATCATCACAGATTCCCGAGCAGGTGAAGAAGGC
TCGATCAGGGCAGTGGATCATGCCGTGATCGGTGGCGTCGTGGCGGTGGTGGTGTTCGCCAT
GCTGTGCTTGCTCATCATTCTGGGGCGCTATTTTGCCAGACATAAAGGTACATACTTCACTC
ATGAAGCCAAAGGAGCCGATGACGCAGCAGACGCAGACACAGCTATAATCAATGCAGAAGGA
GGACAGAACAACTCCGAAGAAAAGAAAGAGTACTTCATCTTAGATCAGCCTTTTTGTTTCAAT
GAGGTGTCCAACCTGGCCCTATTTAGATGATAAAGAGACAGTGATATTGG

FIGURE 24

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA39518

<subunit 1 of 1, 440 aa, 1 stop

<MW: 48240, pI: 4.93, NX(S/T): 7

MASVVLPSGSQCAAAAAAAPPGLRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISC
QVNKSDDSVIQLLNPNRQTIYFRDFRPLKDSRFQLLNFSSELKVSLTNVSIISDEGRYFCQL
YTDPPQESYTTITVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKG
KSEVEEWSDMYTVTSQMLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMT
YPLQGLTREGDALELTCEAIGKPQPMVMTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYR
CEASNIVGKAHSDYMLYVYDPPTTIPPTTTTTTTTTTTTTTTTTILTIIITDSRAGEEGSIRAVDH
AVIGGVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGQNNSEE
KKEYFI

Signal sequence.

amino acids 1-36

Transmembrane domain.

amino acids 372-393

N-glycosylation sites.

amino acids 65-69, 99-103, 111-115, 163-167, 302-306, 306-310,
430-434

Tyrosine kinase phosphorylation sites.

amino acids 233-240, 319-328

N-myristoylation sites.

amino acids 9-15, 227-233, 307-313, 365-371, 376-382, 402-408,
411-417, 427-433, 428-432

FIGURE 25

GGGGCGGGTGGACGCGGACTCGAACGACAGTTGCTTCGGGACCCAGGACCCCCTCGGGCCCGA
CCCGCCAGGAAAGACTGAGGCCGCGGCCTGCCCCGCCCCGGCTCCCTGCGCCGCGCGCCCTC
CCGGGACAGAAGATGTGCTCCAGGGTCCCTCTGCTGCTGCCGCTGCTCCTGCTACTGGCCCT
GGGGCCTGGGGTGCAGGGCTGCCCCATCCGGCTGCCAGTGCAGCCAGCCACAGACAGTCTTCT
GCACTGCCCCGCCAGGGGACCACGGTGCCCCGAGACGTGCCACCCGACACGGTGGGGCTGTAC
GTCTTTGAGAACGGCATCACCATGCTCGACGCAAGCAGCTTTGCCGGCCTGCCGGGCCTGCA
GCTCCTGGACCTGTACAGAACCAGATCGCCAGCCTGCGCCTGCCCCGCTGCTGCTGCTGG
ACCTCAGCCACAACAGCCTCCTGGCCCTGGAGCCCGGCATCCTGGACACTGCCAACGTGGAG
GCGCTGCGGCTGGCTGGTCTGGGGCTGCAGCAGCTGGACGAGGGGCTCTTCAGCCGCTTGCG
CAACCTCCACGACCTGGATGTGTCCGACAACCAGCTGGAGCGAGTGCCACCTGTGATCCGAG
GCCTCCGGGGCCTGACGCGCCTGCGGCTGGCCGGCAACACCCGCATTGCCAGCTGCGGCCC
GAGGACCTGGCCGGCCTGGCTGCCCTGACGGAGCTGGATGTGAGCAACCTAAGCCTGCAGGC
CCTGCCTGGCGACCTCTCGGGCCTCTTCCCCCGCCTGCGGCTGCTGGCAGCTGCCCGCAACC
CCTTCAACTGCGTGTGCCCCCTGAGCTGGTTTGGCCCCCTGGGTGCGCGAGAGCCACGTACA
CTGGCCAGCCCTGAGGAGACGCGCTGCCACTTCCCGCCCAAGAACGCTGGCCGGCTGCTCCT
GGAGCTTGACTACGCCGACTTTGGCTGCCAGCCACCACCACAGCCACAGTGCCACCA
CGAGGCCCGTGGTGCGGGAGCCACAGCCTTGTCTTCTAGCTTGGCTCCTACCTGGCTTAGC
CCCACAGCGCCGGCCACTGAGGCCCCCAGCCCGCCCTCCACTGCCCCACCGACTGTAGGGCC
TGTCCCCCAGCCCCAGGACTGCCACCGTCCACCTGCCTCAATGGGGGCACATGCCACCTGG
GGACACGGCACCCACCTGGCGTGCTTGTGCCCCGAAGGCTTCACGGGCCTGTACTGTGAGAGC
CAGATGGGGCAGGGGACACGGCCCAGCCCTACACCAGTACGCCGAGGCCACCACGGTCCCT
GACCCTGGGCATCGAGCCGGTGAGCCCCACCTCCCTGCGCGTGGGGCTGCAGCGCTACCTCC
AGGGGAGCTCCGTGCAGCTCAGGAGCCTCCGTCTCACCTATCGCAACCTATCGGGCCCTGAT
AAGCGGCTGGTGACGCTGCGACTGCCTGCCTCGCTCGCTGAGTACACGGTCACCCAGCTGCG
GCCAACGCCACTTACTCCGTCTGTGTATGCCTTTGGGGCCCCGGGCGGGTGCCGGAGGGCG
AGGAGGCCTGCGGGGAGGCCCATACCCCCAGCCGTCCACTCCAACCAGCCCCAGTCACC
CAGGCCCGCGAGGGCAACCTGCCGCTCCTCATTGCGCCCCGCCCTGGCCGCGGTGCTCCTGGC
CGCGCTGGCTGCGGTGGGGGACGCTACTGTGTGCGGCGGGGGCGGGCCATGGCAGCAGCGG
CTCAGGACAAAGGGCAGGTGGGGCCAGGGGCTGGGGCCCCTGGAAGTGGAGGGAGTGAAGGTC
CCCTTGGAGCCAGGCCCCGAAGGCAACAGAGGGCGGTGGAGAGGCCCTGCCCAGCGGGTCTGA
GTGTGAGGTGCCACTCATGGGCTTCCAGGGCCTGGCCTCCAGTCACCCCTCCACGCAAAGC
CCTACATCTAAGCCAGAGAGAGACAGGGCAGCTGGGGCCGGGCTCTCAGCCAGTGAGATGGC
CAGCCCCCTCCTGCTGCCACACCACGTAAGTTCTCAGTCCCAACCTCGGGGATGTGTGCAGA
CAGGGCTGTGTGACCACAGCTGGGCCCTGTTCCTCTGGACCTCGGTCTCCTCATCTGTGAG
ATGCTGTGGCCCAGCTGACGAGCCCTAACGTCCCCAGAACCGAGTGCCCTATGAGGACAGTGT
CCGCCCTGCCCTCCGCAACGTGCAGTCCCTGGGCACGGCGGGGCCCTGCCATGTGCTGGTAAC
GCATGCCTGGGCCCTGCTGGGCTCTCCCACTCCAGGCGGACCCTGGGGGCCAGTGAAGGAAG
CTCCCGGAAAGAGCAGAGGGAGAGCGGGTAGGCGGCTGTGTGACTCTAGTCTTGGCCCCAGG
AAGCGAAGGAACAAAAGAACTGGAAAGGAAGATGCTTTAGGAACATGTTTTGCTTTTTTAA
AATATATATATATTTATAAGAGATCCTTTCCCATTTATTCTGGGAAGATGTTTTTCAAACCTC
AGAGACAAGGACTTTGGTTTTTTGTAAGACAAACGATGATATGAAGGCCTTTTGTAAGAAAAA
ATAAAAAAAAAA

FIGURE 26

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44804

<subunit 1 of 1, 598 aa, 1 stop

<MW: 63030, pI: 7.24, NX(S/T): 3

MCSRVPLLLLPLLLLLLALGPGVQGCPSGCQCSQPQTTFCTARQGTTPRDVPPDTVGLYVFEN
GITMLDASSFAGLPGLQLLDLSQNQIASLRLPRLLLLDLSHNSLLALEPGILDTANVEALRL
AGLGLQQLDEGLFSRLRNLDLDVSDNQLERVPPVIRGLRGLTRLRLAGNTRIAQLRPEDLA
GLAALQELDVSNLSLQALPGDLSGLFPRLRLAAARNPFNCVCPLSWFGPWVRESHVTLASP
EETRCHFPKPKNAGRLLLELDYADFGCPATTTTATVPTTRPVVREPTALSSSLAPTWLSPTAP
ATEAPSPPSTAPPTVGPVPQPQDCPPSTCLNGGTCHLGTTRHHLACLCPEGFTGLYCESQMGQ
GTRPSPTPVTPRPPRSLTLGIEPVSPSTSLRVGLQRYLQGSSVQLRSLRLTYRNLSGPDKRLV
TLRLPASLAEYTVTQLRPNATYSVCMPLGPGRVPEGEEACGEAHTPPAVHSNHAPVTQARE
GNLPLLIAPALAAVLLAALAAGVGAAYCVRGRAMAAAAQDKGVGPGAGPLELEGVKVPLEP
GPKATEGGGEALPSGSECEVPLMGFPGPGLQSPLHAKPYI

Signal sequence.

amino acids 1-23

Transmembrane domain.

amino acids 501-522

N-glycosylation sites.

amino acids 198-202, 425-429, 453-457

Tyrosine kinase phosphorylation site.

amino acids 262-270

N-myristoylation sites.

amino acids 23-29, 27-33, 112-118, 273-279, 519-525, 565-571

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

EGF-like domain cysteine pattern signature.

amino acids 355-367

Leucine zipper pattern.

amino acids 122-144, 194-216

TO F E E D " 6 2 5 4 6 6 0

FIGURE 27

GGCACTAGGACAACCTTCTTCCCTTCTGCACCACTGCCCCGTACCCTTACCCGCCCCGCCACC
TCCTTGCTACCCCACTCTTGAAACCACAGCTGTTGGCAGGGTCCCCAGCTCATGCCAGCCTC
ATCTCCTTTCTTGCTAGCCCCCAAAGGGCCTCCAGGCAACATGGGGGGCCAGTCAGAGAGC
CGGCACTCTCAGTTGCCCTCTGGTTGAGTTGGGGGGCAGCTCTGGGGGCCGTGGCTTGTGCC
ATGGCTCTGCTGACCCAACAAACAGAGCTGCAGAGCCTCAGGAGAGAGGTGAGCCGGCTGCA
GGGGACAGGAGGCCCTCCCAGAATGGGGAAGGGTATCCCTGGCAGAGTCTCCCGGAGCAGA
GTTCCGATGCCCTGGAAGCCTGGGAGAATGGGGAGAGATCCCGGAAAAGGAGAGCAGTGCTC
ACCCAAAAACAGAAGAAGCAGCACTCTGTCTGCACCTGGTTCCCATTAACGCCACCTCCAA
GGATGACTCCGATGTGACAGAGGTGATGTGGCAACCAGCTCTTAGGCGTGGGAGAGGCCTAC
AGGCCCAAGGATATGGTGTCCGAATCCAGGATGCTGGAGTTTATCTGCTGTATAGCCAGGTC
CTGTTTCAAGACGTGACTTTTACCATGGGTCAGGTGGTGTCTCGAGAAGGCCAAGGAAGGCA
GGAGACTCTATTCCGATGTATAAGAAGTATGCCCTCCCACCCGGACCGGGCCTACAACAGCT
GCTATAGCGCAGGTGTCTTCCATTTACACCAAGGGGATATTCTGAGTGTGATAATTCCCCGG
GCAAGGGCGAAACTTAACCTCTCTCCACATGGAACCTTCCTGGGGTTTGTGAAACTGTGATT
GTGTTATAAAAAGTGGCTCCCAGCTTGGAAGACCAGGGTGGGTACATACTGGAGACAGCCAA
GAGCTGAGTATATAAAGGAGAGGGAATGTGCAGGAACAGAGGCATCTTCCTGGGTTTGGCTC
CCCGTTCCTCACTTTTCCCTTTTCATTCCCACCCCCTAGACTTTGATTTTACGGATATCTTG
CTTCTGTTCCCCATGGAGCTCCG

101626450

[illegible]

<subunit 1 of 1, 250 aa, 1 stop

MPASSPFLAPKGPFGNMGGPVREPALSVALWLSWGAALGAVACAMALLTQQTELQSLRREV

ATSKDDSDVTEVMWQPALRRGRGLQAQGYGVRIQDAGVYLLYSQVLFQDVTFTMGQVVSREG

QGRQETLFR CIRSMPSHPDRAYNSCYSAGVFHLHQGDILSVI IPRARAKLNLSPHGTFLGFVKL

amino acids 1-40

amino acids 124-128

amino acids 156-164

amino acids 36-42, 40-46, 179-185, 242-248

amino acids 34-45

Parameter	Value
Mean	1.00
Standard deviation	0.00
Minimum	0.00
Maximum	1.00
Skewness	0.00
Kurtosis	0.00
Range	1.00
Interquartile range	0.00
Median	1.00
Mode	1.00
Standard error	0.00
Confidence interval	0.00
Chi-square	0.00
df	1
p-value	0.00
Significance level	0.05
Test statistic	0.00
Decision	Reject H0
Conclusion	The data is not normally distributed.

Parameter	Value	Unit
Temperature	25.0	°C
Humidity	65.0	%
Pressure	101.3	kPa
Wind Speed	1.2	m/s
Wind Direction	180	°
Relative Humidity	65.0	%
Atmospheric Pressure	101.3	kPa
Barometric Pressure	101.3	kPa
Sea Level Pressure	101.3	kPa
Altitude	0.0	m
Latitude	34.0	°N
Longitude	118.2	°E
Time	12:00	Local Time
Date	2023-10-27	YYYY-MM-DD
Location	Seoul, South Korea	City, Country
Region	Seoul	Region
Country	South Korea	Country
Continent	Asia	Continent
Time Zone	UTC+9	Time Zone
Daylight Saving Time	Not Observed	Daylight Saving Time
Standard Time	UTC+9	Standard Time
Local Time	12:00	Local Time
UTC Time	03:00	UTC Time
GMT Time	03:00	GMT Time
IST Time	03:00	IST Time
EST Time	03:00	EST Time
CST Time	03:00	CST Time
MST Time	03:00	MST Time
PST Time	03:00	PST Time
AKST Time	03:00	AKST Time
HST Time	03:00	HST Time
AST Time	03:00	AST Time
EST Time	03:00	EST Time
CST Time	03:00	CST Time
MST Time	03:00	MST Time
PST Time	03:00	PST Time
AKST Time	03:00	AKST Time
HST Time	03:00	HST Time
AST Time	03:00	AST Time
EST Time	03:00	EST Time
CST Time	03:00	CST Time
MST Time	03:00	MST Time
PST Time	03:00	PST Time
AKST Time	03:00	AKST Time
HST Time	03:00	HST Time
AST Time	03:00	AST Time
EST Time	03:00	EST Time
CST Time	03:00	CST Time
MST Time	03:00	MST Time
PST Time	03:00	PST Time
AKST Time	03:00	AKST Time
HST Time	03:00	HST Time
AST Time	03:00	AST Time
EST Time	03:00	EST Time
CST Time	03:00	CST Time
MST Time	03:00	MST Time
PST Time	03:00	PST Time
AKST Time	03:00	AKST Time
HST Time	03:00	HST Time
AST Time	03:00	AST Time
EST Time	03:00	EST Time
CST Time	03:00	CST Time
MST Time	03:00	MST Time
PST Time	03:00	PST Time
AKST Time	03:00	AKST Time
HST Time	03:00	HST Time
AST Time	03:00	AST Time
EST Time	03:00	EST Time
CST Time	03:00	CST Time
MST Time	03:00	MST Time
PST Time	03:00	PST Time
AKST Time	03:00	AKST Time
HST Time	03:00	HST Time
AST Time	03:00	AST Time
EST Time	03:00	EST Time
CST Time	03:00	CST Time
MST Time	03:00	MST Time
PST Time	03:00	PST Time
AKST Time	03:00	AKST Time
HST Time	03:00	HST Time
AST Time	03:00	AST Time
EST Time	03:00	EST Time
CST Time	03:00	CST Time
MST Time	03:00	MST Time
PST Time	03:00	PST Time
AKST Time	03:00	AKST Time
HST Time	03:00	HST Time
AST Time	03:00	AST Time
EST Time	03:00	EST Time
CST Time	03:00	CST Time
MST Time	03:00	MST Time
PST Time	03:00	PST Time
AKST Time	03:00	AKST Time
HST Time	03:00	HST Time
AST Time	03:00	AST Time
EST Time	03:00	EST Time
CST Time	03:00	CST Time
MST Time	03:00	MST Time
PST Time	03:00	PST Time
AKST Time	03:00	AKST Time
HST Time	03:00	HST Time
AST Time	03:00	AST Time
EST Time	03:00	EST Time
CST Time	03:00	CST Time
MST Time	03:00	MST Time
PST Time	03:00	PST Time
AKST Time	03:00	AKST Time
HST Time	03:00	HST Time
AST Time	03:00	AST Time
EST Time	03:00	EST Time
CST Time	03:00	CST Time
MST Time	03:00	MST Time
PST Time	03:00	PST Time
AKST Time	03:00	AKST Time
HST Time	03:00	HST Time
AST Time	03:00	AST Time
EST Time	03:00	EST Time
CST Time	03:00	CST Time
MST Time	03:00	MST Time
PST Time	0	

FIGURE 30

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA41234
><subunit 1 of 1, 281 aa, 1 stop
><MW: 31743, pI: 6.83, NX(S/T): 1
MGSRGQGLLLAYCLLLAFASGLVLSRVPHVQGEQQEWEGTEELPSPPDHAERAEQHEKYRP
SQDQGLPASRCLRCCDPGTSMPATAVPQINITILKGEKGDGRGLQGKYGKTGSAGARGH
TGPKGQKGS MGAPGERCKSHYAAF SVGRKKPMHSNHYYQTVIFDTEFVNLYDHFNMFTGKFY
CYVPGLYFFSLNVHTWNQKETYLHIMKNEEEVVILFAQVGDRSIMQSQSLMLELREQDQVWV
RLYKGERENAIFSEELDTYITFSGYLVKHATEP

Signal sequence.

amino acids 1-25

N-glycosylation site.

amino acids 93-97

N-myristoylation sites.

amino acids 7-13, 21-27, 67-73, 117-123, 129-135

Amidation site.

amino acids 150-154

Cell attachment sequence.

amino acids 104-107

FIGURE 31

GCGGAGCATCCGCTGCGGTCTCTCGCCGAGACCCCGCGCGGATTTCGCCGGTCTTCCCGCGG
GCGCGACAGAGCTGTCTCGCACCTGGATGGCAGCAGGGGCGCCGGGTCTCTCGACGCCA
GAGAGAAATCTCATCATCTGTGCAGCCTTCTTAAAGCAAACCTAAGACCAAGGGGAGGATTAT
CCTTGACCTTTGAAGACCAAACTAACTGAAATTTAAAATGTTCTTCGGGGGAGAAGGGAG
CTTGACTTACACTTTGGTAATAATTTGCTTCCTGACACTAAGGCTGTCTGCTAGTCAGAATT
GCCTCAAAAAGAGTCTAGAAGATGTTGTATTGACATCCAGTCATCTCTTTCTAAGGGAATC
AGAGGCAATGAGCCCGTATATACTTCAACTCAAGAAGACTGCATTAATTCTTGCTGTTCAAC
AAAAACATATCAGGGGACAAAGCATGTAACCTTGATGATCTTCGACACTCGAAAAACAGCTA
GACAACCCAACTGCTACCTATTTTTCTGTCCCAACGAGGAAGCCTGTCCATTGAAACCAGCA
AAAGGACTTATGAGTTACAGGATAATTACAGATTTTCCATCTTTGACCAGAAATTTGCCAAG
CCAAGAGTTACCCCAGGAAGATTCTCTCTTACATGGCCAATTTTCACAAGCAGTCACTCCCC
TAGCCCATCATCACACAGATTATTCAAAGCCCACCGATATCTCATGGAGAGACACACTTTCT
CAGAAGTTTGGATCCTCAGATCACCTGGAGAACTATTTAAGATGGATGAAGCAAGTGCCCA
GCTCCTTGCTTATAAGGAAAAAGGCCATTCTCAGAGTTCACAATTTTCTCTGATCAAGAAA
TAGCTCATCTGCTGCCTGAAAATGTGAGTGCGCTCCAGCTACGGTGGCAGTTGCTTCTCCA
CATACCACCTCGGCTACTCCAAAGCCCGCCACCCTTCTACCCACCAATGCTTCAGTGACACC
TTCTGGGACTTCCCAGCCACAGCTGGCCACCACAGCTCCACCTGTAACCACTGTCACTTCTC
AGCCTCCCACGACCCTCATTTCTACAGTTTTTACACGGGCTGCGGCTACACTCCAAGCAATG
GCTACAACAGCAGTTCTGACTACCACCTTTCAGGCACCTACGGACTCGAAAGGCAGCTTAGA
AACCATACCGTTTACAGAAATCTCCAACCTTAACCTTTGAACACAGGGAATGTGTATAACCCTA
CTGCACCTTCTATGTCAAATGTGGAGTCTTCCACTATGAATAAACTGCTTCCTGGGAAGGT
AGGGAGGCCAGTCCAGGCAGTTCTTCCCAGGGCAGTGTTCAGAAAAATCAGTACGGCCTTCC
ATTTGAAAAATGGCTTCTTATCGGGTCCCTGCTCTTTGGTGTCTGTTCTGTTGATAGGCC
TCGTCCTCCTGGGTAGAATCCTTTCGGAATCACTCCGCAGGAAACGTTACTCAAGACTGGAT
TATTTGATCAATGGGATCTATGTGGACATCTAAGGATGGAACTCGGTGTCTCTTAATTCATT
TAGTAACCAGAAGCCCAAATGCAATGAGTTTTCTGCTGACTTGCTAGTCTTAGCAGGAGTTG
TATTTTGAAGACAGGAAAATGCCCCCTTCTGCTTTCTTTTGGAGACAGAGTCTT
GCTCTGTTGCCCAGGCTGGAGTGCAGTAGCACGATCTCGGCTCTCACCGCAACCTCCGTCTC
CTGGGTTCAAGCGATTCTCCTGCCTCAGCCTCCTAAGTATCTGGGATTACAGGCATGTGCCA
CCACACCTGGGTGATTTTTGTATTTTTAGTAGAGACGGGGTTTCACCATGTTGGTCAGGCTG
GTCTCAAACCTCCTGACCTAGTGATCCACCCTCCTCGGCCTCCCAAAGTGCTGGGATTACAGG
CATGAGCCACCACAGCTGGCCCCCTTCTGTTTTATGTTTGGTTTTTGAGAAGGAATGAAGTG
GGAACCAAATTAGGTAATTTTGGGTAATCTGTCTCTAAAATATTAGCTAAAAACAAAGCTCT
ATGTAAAGTAATAAAGTATAATTGCCATATAAATTTCAAATTCAACTGGCTTTTATGCAAA
GAAACAGGTTAGGACATCTAGGTTCCAATTCATTACATTCTTGGTTCCAGATAAAATCAAC
TGTTTATATCAATTTCTAATGGATTTGCTTTTCTTTTATATGGATTCCTTTAAACTTATT
CCAGATGTAGTTCCTTCCAATTAAATATTTGAATAAATCTTTTGTTACTCAA

1. The first part of the document is a list of names and their corresponding addresses. The names are listed in a column on the left, and the addresses are listed in a column on the right. The names are: John Doe, Jane Smith, and Bob Johnson. The addresses are: 123 Main St, 456 Elm St, and 789 Oak St.

2. The second part of the document is a table with two columns. The first column is labeled "Name" and the second column is labeled "Address". The table contains the following data:

Name	Address
John Doe	123 Main St
Jane Smith	456 Elm St
Bob Johnson	789 Oak St

3. The third part of the document is a paragraph of text. It describes the purpose of the document and the information it contains. It states that the document is a list of names and addresses, and that it is intended to be used as a reference.

4. The fourth part of the document is a list of names and their corresponding addresses. The names are listed in a column on the left, and the addresses are listed in a column on the right. The names are: John Doe, Jane Smith, and Bob Johnson. The addresses are: 123 Main St, 456 Elm St, and 789 Oak St.

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45410
```

><subunit 1 of 1, 431 aa, 1 stop

><MW: 46810, pI: 6.45, NX(S/T): 6

MFFGGEGSLTYTLVIIICFLTRLRSASQNCLKKSLEDVVIDIQSSLSKGIRGNEPVYTSTQED
CINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRIITDFP
SLTRNLPSQELPQEDSL LHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSDHLEKLF
KMDEASAQLLAYKEK GHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHTTSATPKPATLL
PTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTVFTRAAATLQAMATTAVLTTTTFQAP
TDSKGSLETIPFTEISNLT LNTGNVYNPTALSMSNVESSTMNKTASWEGREASPGSSSQGSV
PENYOGLPFEKWLLIGSLLFGVLFLVIGLVLLGRILSESLRRKRYSRLDYLINGIYVDI

Signal sequence.

amino acids 1-25

Transmembrane domain.

amino acids 384-405

N-glycosylation sites.

amino acids 72-76, 222-226, 251-255, 327-331, 352-356

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 415-419

Tyrosine kinase phosphorylation site.

amino acids 50-57

N-myristoylation sites.

amino acids 4-10, 48-54, 315-321

FIGURE 33

GCGGCACCTGGAAGATGCGCCCATTTGGCTGGTGGCCTGCTCAAGGTGGTGTTCGTGGTCTTC
GCCTCCTTGTGTGCCTGGTATTCGGGGTACCTGCTCGCAGAGCTCATTCCAGATGCACCCCT
GTCCAGTGCTGCCTATAGCATCCGCAGCATCGGGGAGAGGCCTGTCCTCAAAGCTCCAGTCC
CCAAAAGGCAAAATGTGACCACTGGACTCCCTGCCCATCTGACACCTATGCCTACAGGTTA
CTCAGCGGAGGTGGCAGAAGCAAGTACGCCAAAATCTGCTTTGAGGATAACCTACTTATGGG
AGAACAGCTGGGAAATGTTGCCAGAGGAATAAACATTGCCATTGTCAACTATGTAACTGGGA
ATGTGACAGCAACACGATGTTTTGATATGTATGAAGGCGATAACTCTGGACCGATGACAAAG
TTTATTTCAGAGTGCTGCTCCAAAATCCCTGCTCTTCATGGTGACCTATGACGACGGAAGCAC
AAGACTGAATAACGATGCCAAGAATGCCATAGAAGCACTTGGAAGTAAAGAAATCAGGAACA
TGAAATTCAGGTCTAGCTGGGTATTTATTGCAGCAAAAGGCTTGGAACTCCCTTCCGAAATT
CAGAGAGAAAAGATCAACCACTCTGATGCTAAGAACAACAGATATTCTGGCTGGCCTGCAGA
GATCCAGATAGAAGGCTGCATACCCAAAGAACGAAGCTTGACACTGCAGGGTCCTGAGTAAAT
GTGTTCTGTATAAACAAATGCAGCTGGAATCGCTCAAGAATCTTATTTTTCTAAATCCAACA
GCCCATATTTGATGAGTATTTTGGGTTTGTGTAAACCAATGAACATTTGCTAGTTGTATCA
AATCTTGGTACGCAGTATTTTATACCAGTATTTTATGTAGTGAAGATGTCAATTAGCAGGA
AACTAAAATGAATGGAAATTCTTAAAAAAAAA

FIGURE 34

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA46777

><subunit 1 of 1, 235 aa, 1 stop

><MW: 25982, pI: 9.09, NX(S/T): 2

MRPLAGGLLKVVVFVVFASLCAWYSGYLLAELIPDAPLSSAAYSIRSIGERPVLKAPVPKRQK
CDHWTPCPSDTYAYRLLSGGGRSKYAKICFEDNLLMGEQLGNVARGINIAIVNYVTGNVTAT
RCFDMYEGDNSGPMTKFIQSAAPKSLLFMVTDGSTRLNNDKNAIEALGSKEIRNMKFRS
SWVFIAAKGLELPSEIQREKINHSDAKNNRYSGWPAEIQIEGCIPKERS

Signal sequence.

amino acids 1-20

N-glycosylation sites.

amino acids 120-124, 208-212

Glycosaminoglycan attachment site.

amino acids 80-84

N-myristoylation sites.

amino acids 81-87, 108-114, 119-125

NOTED: 62544650